

TGAAGTCTCTCCCAAGCAAATGGGAGCTTCTTTGGACCTTGGAGCACACAGAGGATTCTACTTTCTTTAAACTTTGTT 80

TTCAGGCAATTTCCCTGAGAACCGTTTACTTCCAGAAGATTGGTGGAGCTTGATCTGAAGGCTGGCCATGAAATCTCAAG 160

M K S Q

GTC AACATTGGTATCCAGTTCAGATAAAACTGTAAAGTGAGCTTTCGTGAGAAGCTTCTGATTATTGATTCAAACCTG 240

G Q H W Y S S S D K N C K V S F R E K L L I I D S N L

GGGGTCCAAGATGTGGAGAACCTCAAGTTTCTCTGCATAGGATTGGTCCCCAACAGAAGCTGGAGAAGTCCAGCTCAGC 320

G V Q D V E N L K F L C I G L V P N K K L E K S S S A

CTCAGATGTTTTGAACATCTCTTGGCAGAGGATCTGCTGAGTGAGGAAGACCCCTTCTTCTGGCAGAACTCCTCTATA 400

S D V F E H L L A E D L L S E E D P F F L A E L L Y

TCATACGGCAGAAGAAGCTGCTGCAGCACCTCAACTGTACCAAAGAGGAAGTGGAGCGACTGCTGCCACCCGACAAAGG 480

I I R Q K K L L Q H L N C T K E E V E R L L P T R Q R

GTTTCTCTGTTTAGAAACCTGCTCTACGAACTGTGAGAAGGCATTGACTCAGAGAACTTAAAGGACATGATCTTCTTCT 560

V S L F R N L L Y E L S E G I D S E N L K D M I F L L

GAAAGACTCGCTTCCCAAACTGAAATGACCTCCCTAAGTTTCTGGCATTCTAGAGAAACAAGGTAAAATAGATGAAG 640

K D S L P K T E M T S L S F L A F L E K Q G K I D E

ATAATCTGACATGCCTGGAGGACCTCTGCAAAACAGTTGTACCTAACTTTTGAGAAACATAGAGAAATACAAAAGAGAG 720

D N L T C L E D L C K T V V P K L L R N I E K Y K R E

AAAGCTATCCAGATAGTGACACCTCTGTAGACAAGGAAGCCGAGTCGTATCAAGGAGAGGAAGAACTAGTTTCCCAAC 800

K A I Q I V T P P V D K E A E S Y Q G E E E L V S Q T

Fig. 1A

AGATGTTAAGACATTCTTGAAGCCTTACCGAGGGCAGCTGTGTACAGGATGAATCGGAACCACAGAGGCCTCTGTGTCA 880
D V K T F L E A L P R A A V Y R M N R N H R G L C V
TTGTCAACAACCACAGCTTTACCTCCCTGAAGGACAGACAAGGAACCCATAAAGATGCTGAGATCCTGAGTCATGTGTTC 960
I V N N H S F T S L K D R Q G T H K D A E I L S H V F
CAGTGGCTTGGGTTACAGTGCATATACACAATAATGTGACGAAAGTGGAATGGAGATGGTCCTGCAGAAGCAGAAGTG 1040
Q W L G F T V H I H N N V T K V E M E M V L Q K Q K C
CAATCCAGCCCATGCCGACGGGGACTGCTTCGTGTTCTGTATTCTGACCCATGGGAGATTTGGAGCTGTCTACTCTTCGG 1120
N P A H A D G D C F V F C I L T H G R F G A V Y S S
ATGAGGCCCTCATTCCCATTCGGGAGATCATGTCTCACTTCACAGCCCTGCAGTGGCCTAGACTGGCTGAAAAACCTAAA 1200
D E A L I P I R E I M S H F T A L Q C P R L A E K P K
CTCTTTTTCATCCAGGCCTGCCAAGGTGAAGAGATACAGCCTTCGGTATCCATCGAAGCAGATGCTCTGAACCCTGAGCA 1280
L F F I Q A C Q G E E I Q P S V S I E A D A L N P E Q
GGCACCCACTTCCCTGCAGGACAGTATTCCTGCCGAGGCTGACTTCCTACTTGGTCTGGCCACTGTCCCAGGCTATGTAT 1360
A P T S L Q D S I P A E A D F L L G L A T V P G Y V
CCTTTCGGCATGTGGAGGAAGGCAGCTGGTATATTCACTCTGTGTGAATCATCTGAAGAAATTGGTCCCAAGACATGAA 1440
S F R H V E E G S W Y I Q S L C N H L K K L V P R H E
GACATCTTATCCATCCTCACTGCTGTCAACGATGATGTGAGTGAAGAGTGGACAAACAGGGAACAAAGAAACAGATGCC 1520
D I L S I L T A V N D D V S R R V D K Q G T K K Q M P
CCAGCCTGCTTTCACACTAAGGAAAAAACTAGTATTCCTGTGCCCTGGATGCACTTTCAATATAGCAGAGAGTTTTTG 1600
Q P A F T L R K K L V F P V P L D A L S I
NTGGTCTTAGACCTCAAACGAATCATTGGGNTATAACCTCCAGCCTCCTGCCAGCACAGGAATCGGTGGTCTCCACCTG 1680
TCATTCTAGAAACAGGAAAC 1700

Fig. 1B

TGAAGGCTGGTTGTTCACTGAGCTTTCTGCCTGCCTGTACCCGCCAACAGCTTCAGAAGAAGGTGACTGGTGGCTGC 80
CTGAGGAATACCAGTGGGCAAGAGAATTAGCATTTCTGGAGCATCTGCTGTCTGAGCAGCCCTGGGTGCGTCCACTTTC 160
TGGGCACGTGAGGTTGGGCCTTGGCCGCTGAGCCCTTGAGTTGGTCACTTGAACCTTGGGAAATATTGAGATTATATTCT 240
CCTGCCTTTTAAAAAGATGGACTTCAGCAGAAATCTTTATGATATTGGGGAACAACCTGGACAGTGAAGATCTGGCCTCCC 320
M D F S R N L Y D I G E Q L D S E D L A S
TCAAGTTCCTGAGCCTGGACTACATTCCGCAAAGGAAGCAAGAACCCATCAAGGATGCCTTGATGTTATTCCAGAGACTC 400
L K F L S L D Y I P Q R K Q E P I K D A L M L F Q R L
CAGGAAAAGAGAATGTTGGAGGAAAGCAATCTGTCCTTCTGAAGGAGCTGCTCTTCCGAATTAATAGACTGGATTGCT 480
Q E K R M L E E S N L S F L K E L L F R I N R L D L L
GATTACCTACCTAAACACTAGAAAGGAGGAGATGGAAGGGAACCTCAGACACCAGGCAGGGCTCAAATTTCTGCCTACA 560
I T Y L N T R K E E M E R E L Q T P G R A Q I S A Y
GGTTCACCTTCTGCCGCATGAGCTGGGCTGAAGCAAACAGCCAGTGCCAGACACAGTCTGTACCTTTCTGGCGGAGGGTC 640
R F H F C R M S W A E A N S Q C Q T Q S V P F W R R V
GATCATCTATTAATAAGGGTCATGCTCTATCAGATTCAGAAGAAGTGAGCAGATCAGAATTGAGGTCTTTTAAGTTTCT 720
D H L L I R V M L Y Q I S E E V S R S E L R S F K F L
TTTGCAAGAGGAAATCTCAAATGCAAACCTGGATGATGACATGAACCTGCTGGATATTTTCATAGAGATGGAGAAGAGGG 800
L Q E E I S K C K L D D D M N L L D I F I E M E K R
TCATCCTGGGAGAAGGAAAGTTGGACATCCTGAAAAGAGTCTGTGCCCAAATCAACAAGAGCCTGCTGAAGATAATCAAC 880
V I L G E G K L D I L K R V C A Q I N K S L L K I I N
GACTATGAAGAATTCAGCAAAGGGGAGGAGTTGTGTGGGTAAATGACGATGTCGGAAGTGTCCAAGAGAACAGGATAGTGA 960
D Y E E F S K G E E L C G V M T M S D C P R E Q D S E

Fig. 2A

TCACCGCAAGCTCCGCCTCCGGGTTCAGGCCATTCTCTGCT 1883

Fig. 2B

Consensus

human EADD

Mch4 A

Mch5 A

Mch4 B

Mch5 B

Consensus

human EAADD

Mch4 A

Mch5 A

Mch4 B

Mch5 B

Consensus

human FADD

Mch4 A

Mch5 A

Mch4 B

Mch5 B

Fig. 3A

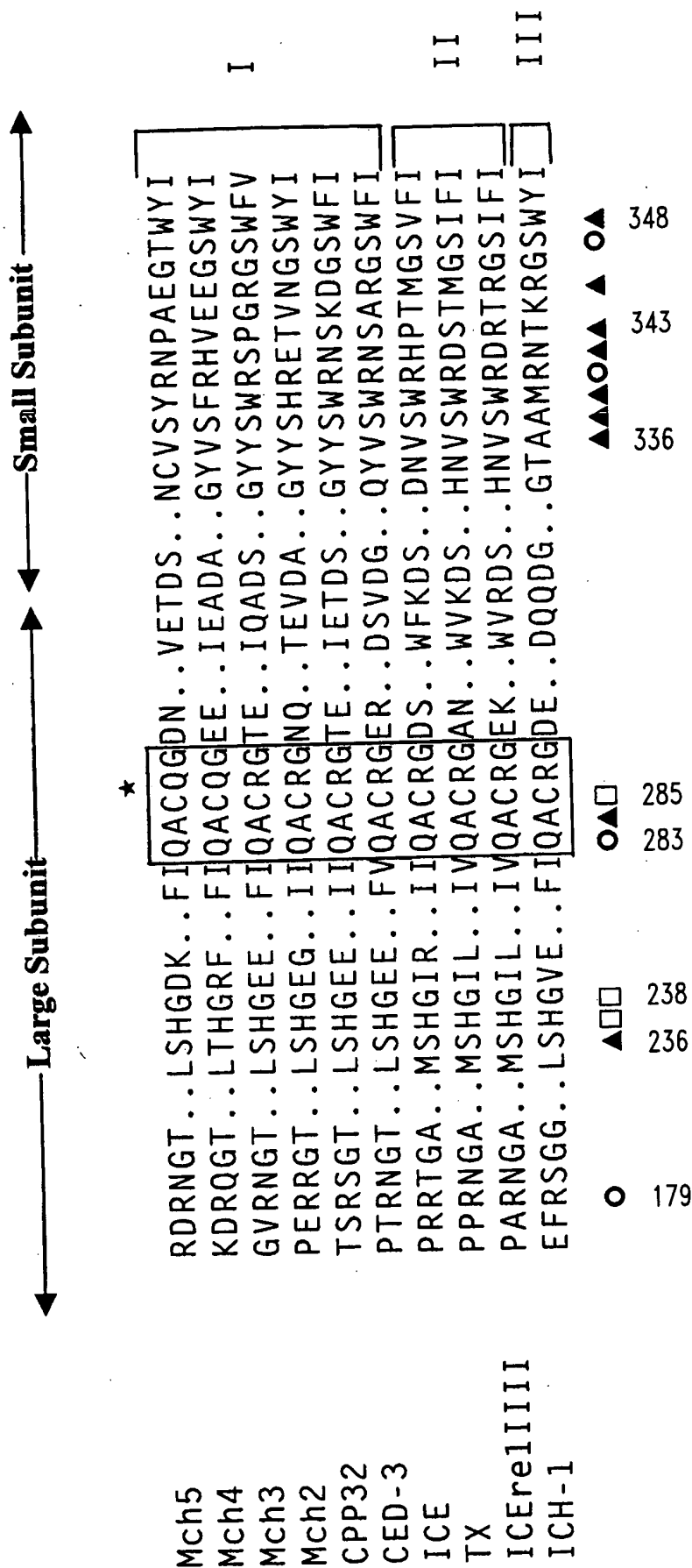


Fig. 3B

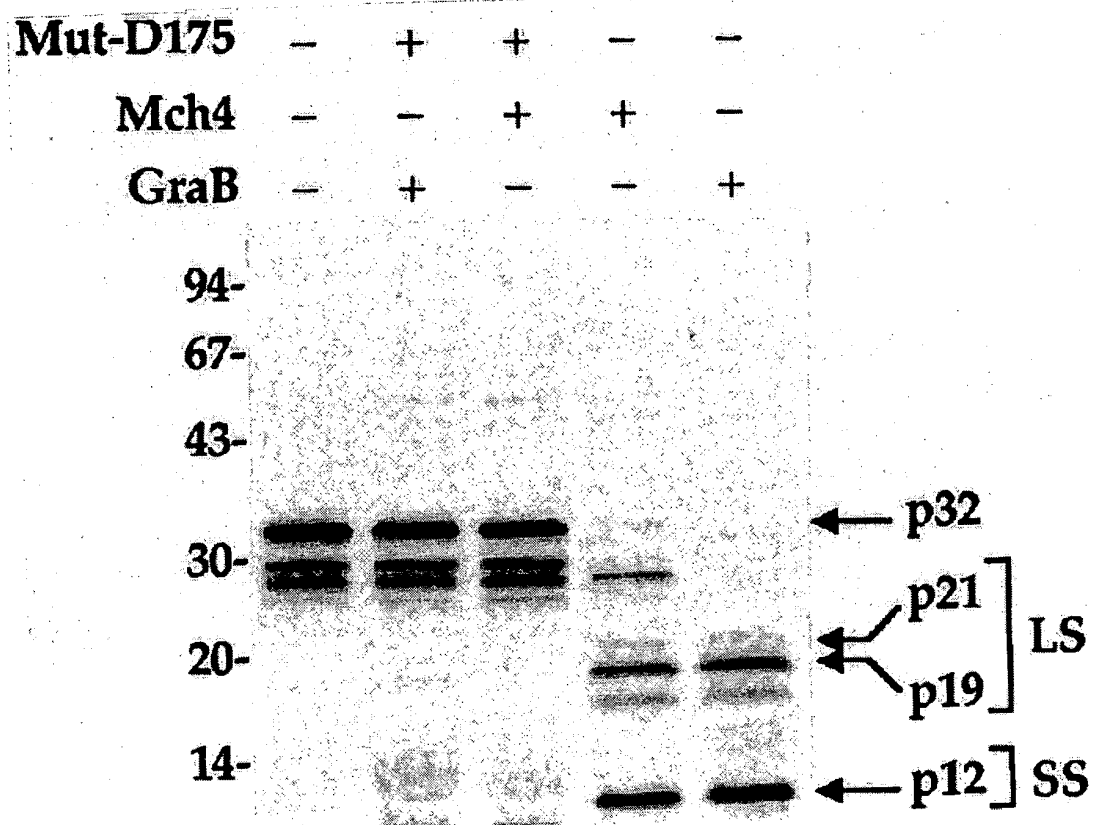


Fig. 4A

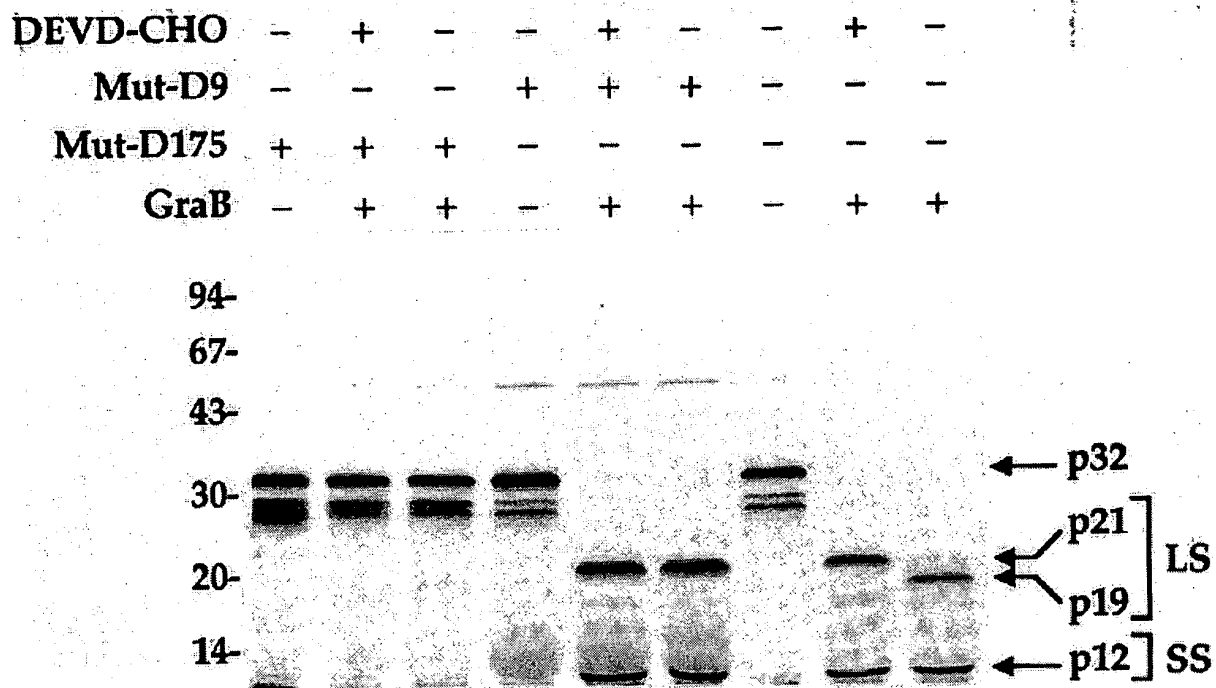


Fig. 4B

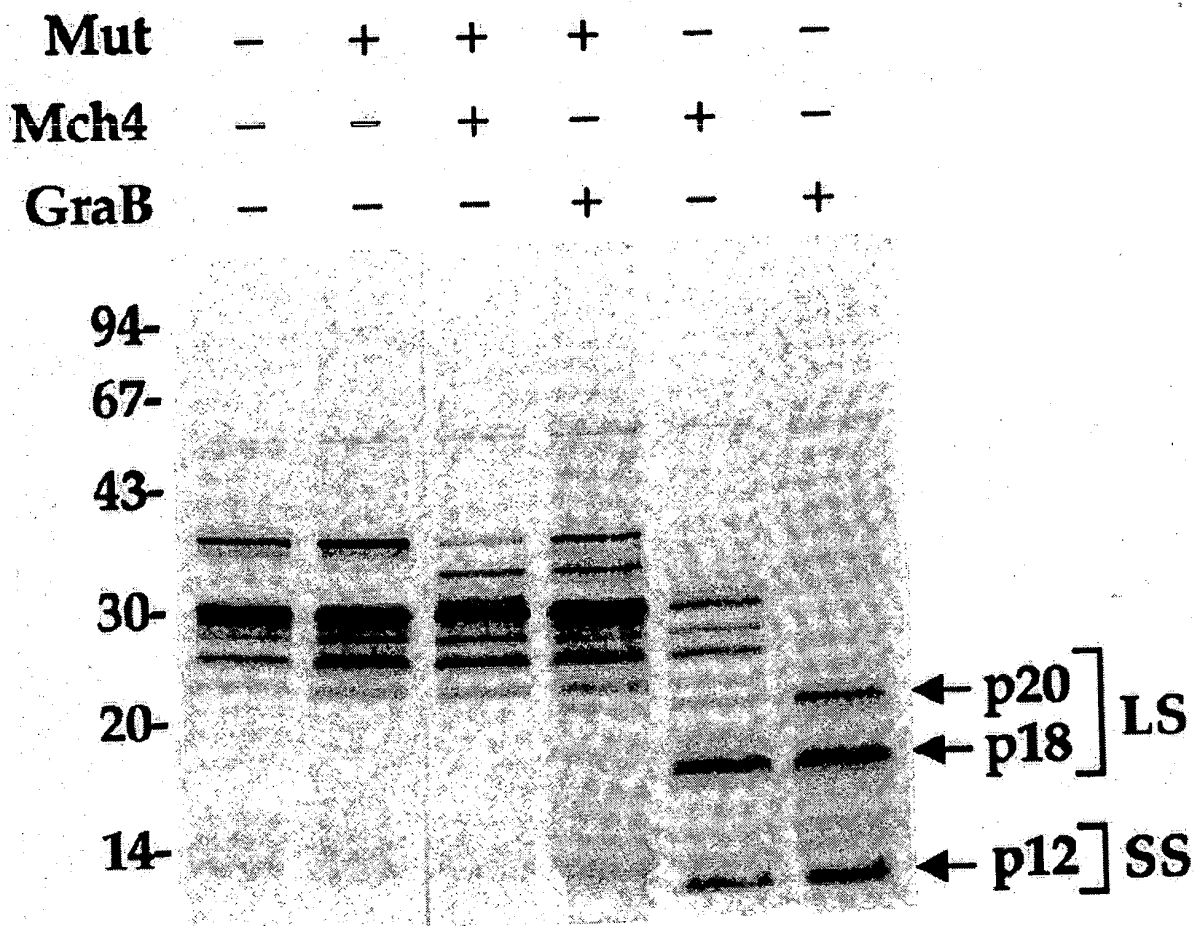


Fig. 5A

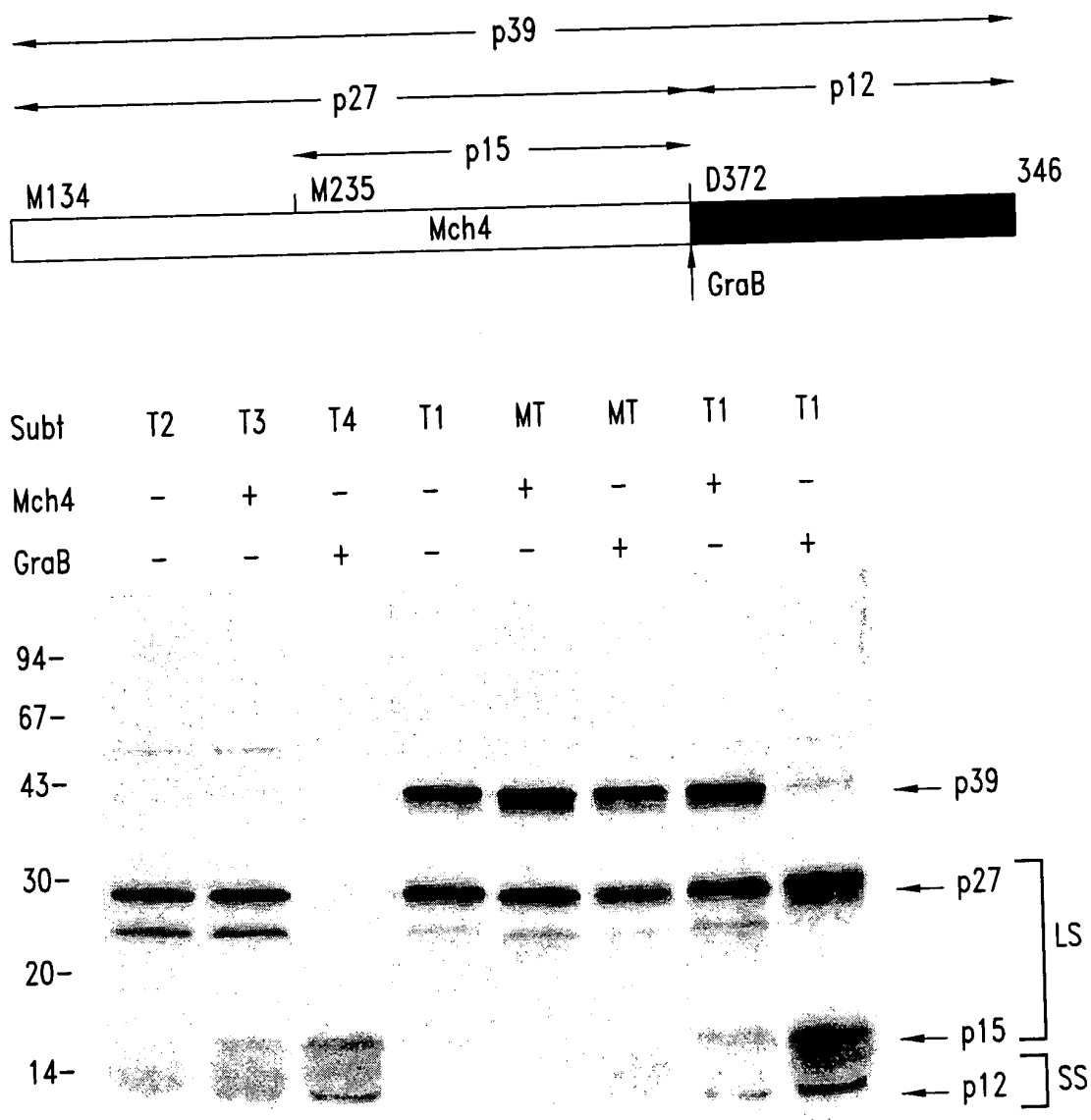


Fig. 5B

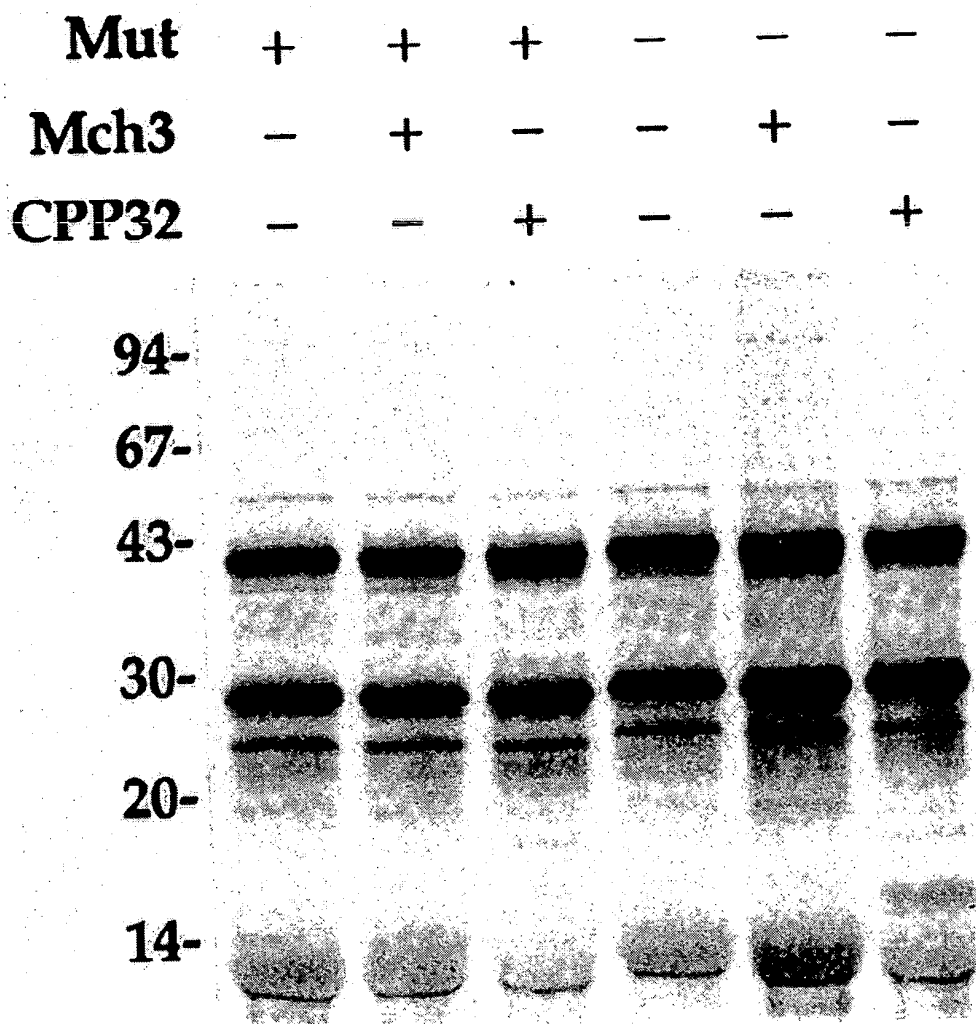


Fig. 6

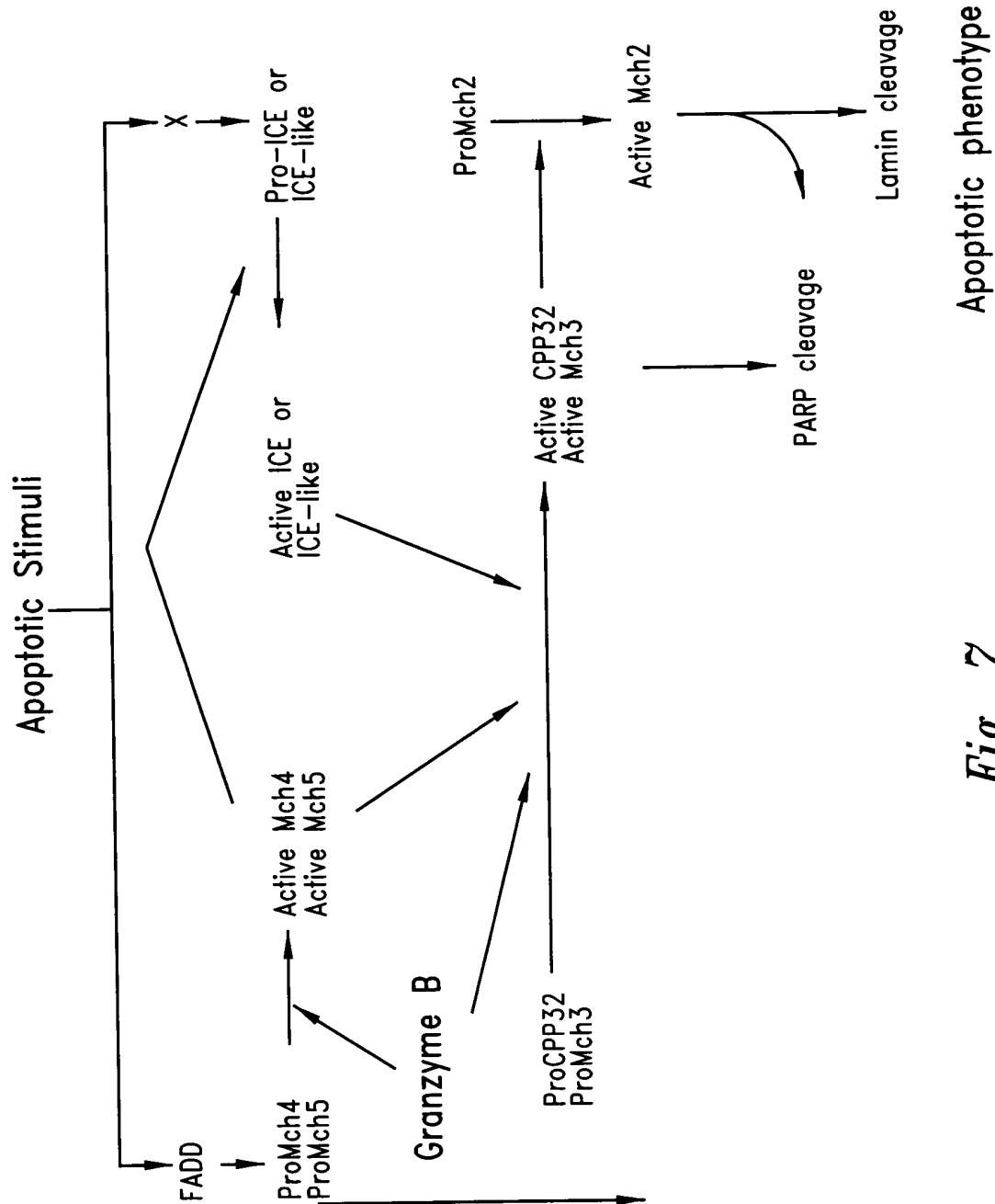


Fig. 7

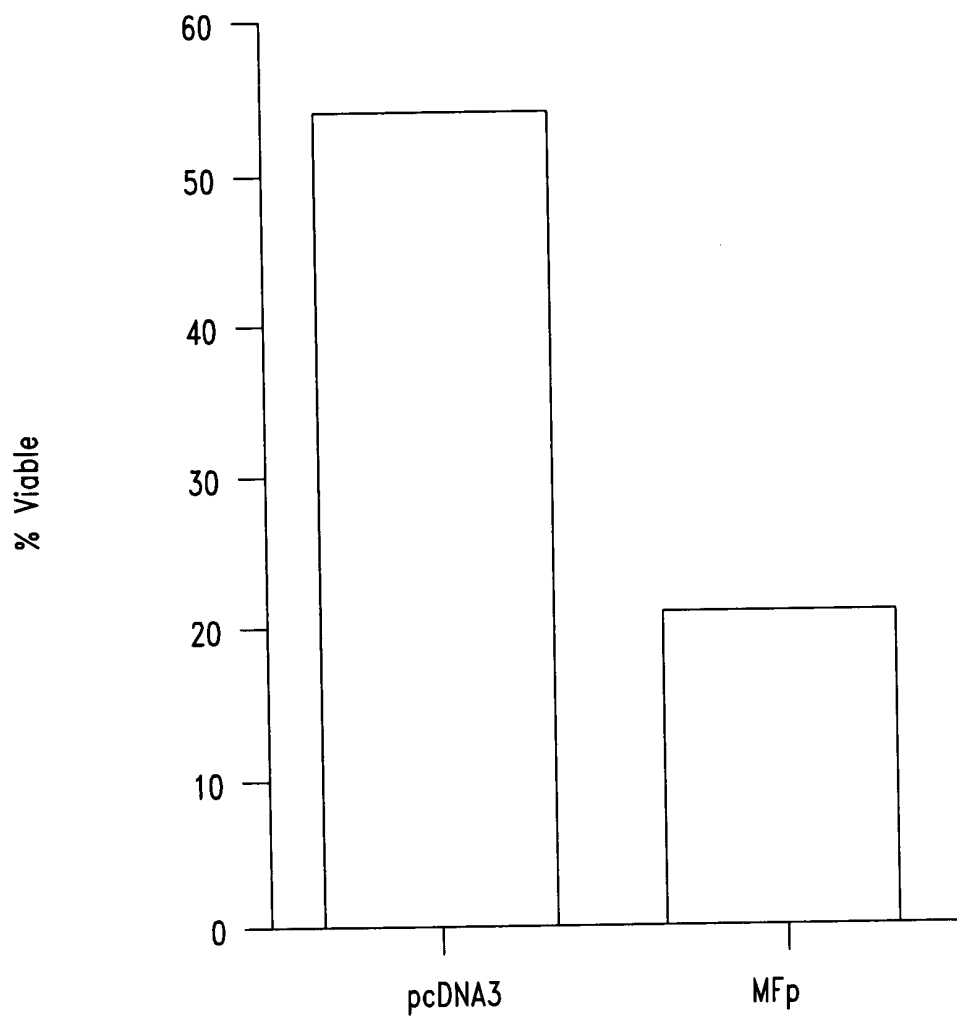


Fig. 8